

CHIR0340.ST25.txt
SEQUENCE LISTING

<110> Knapp, Bernhard
Hundt, Erika
Schmidt, Karl-Heinz

<120> Proteins, In Particular Membrane Proteins, of
Helicobacter Pylori, Their Preparation and Use

<130> CHIR-0340

<140>
<141> Herewith

<150> 09/230,158
<151> 1999-01-19

<150> PCT/IB97/00981
<151> 1997-07-25

<160> 52

<170> PatentIn Ver. 2.1

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<212> PRT
<213> Helicobacter pylori

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<210> 3
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 <223> Unknown Amino Acid, probably Met.

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 <223> Xaa is probably Thr.

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<220>
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Ala Asp Gln Lys Xaa
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<210> 13
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<220>
 <223> urease A

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Gly Glu Leu Ala
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Gln Asn Gln Thr Lys Met Val Asn Asp
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<210> 16
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<222> (334)..(1851)

<223> protein

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<223> catalase from Helicobacter pylori

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cagattaaaa ataaaatttt gtccttaatc tttcttattt tcattaatg ttacgaatag 180
aaataacttaa ggggtttttt taattcttaa aaaaggattt tttaaggaaa ttgaatcttg 240
ttagtctttg tataacaaat tatgtaataa tcaccacaag tgatcggctt agtgtcagat 300
tacgaagatt taagatcaat tacaggaaaa aag atg gtt aat aaa gat gtg aaa 354
                               Met Val Asn Lys Asp Val Lys
                               1           5

caa acc act gct ttt ggc gct ccc gtt tgg gat gac aac aat gtg att 402
Gln Thr Thr Ala Phe Gly Ala Pro Val Trp Asp Asp Asn Asn Val Ile
          10                15                20

acg gcc ggc cct aga ggt cct gtt tta tta caa agc act tgg ttt ttg 450
Thr Ala Gly Pro Arg Gly Pro Val Leu Leu Gln Ser Thr Trp Phe Leu
          25                30                35

gaa aag tta gcg gcg ttt gac aga gaa aga atc cct gaa agg gtg gtg 498
Glu Lys Leu Ala Ala Phe Asp Arg Glu Arg Ile Pro Glu Arg Val Val
          40                45                50                55

cat gct aaa gga agc gga gct tat ggc act ttc act gtg act aaa gac 546
His Ala Lys Gly Ser Gly Ala Tyr Gly Thr Phe Thr Val Thr Lys Asp
          60                65                70

atc act aaa tac act aaa gcg aaa att ttc tct aaa gtg ggc aaa aaa 594
Ile Thr Lys Tyr Thr Lys Ala Lys Ile Phe Ser Lys Val Gly Lys Lys
          75                80                85

acc gaa tgc ttc ttc aga ttt tcc act gtg gct ggt gaa aga ggc agt 642
Thr Glu Cys Phe Phe Arg Phe Ser Thr Val Ala Gly Glu Arg Gly Ser
          90                95                100

gcg gat gcg gta aga gac cct aga ggt ttt gcg atg aag tat tac act 690
Ala Asp Ala Val Arg Asp Pro Arg Gly Phe Ala Met Lys Tyr Tyr Thr
          105                110                115

gaa gaa ggt aac tgg gat tta gta ggg aac aac acg cct gtc ttc ttt 738
Glu Glu Gly Asn Trp Asp Leu Val Gly Asn Asn Thr Pro Val Phe Phe
          120                125                130                135

atc cgt gat gcg atc aaa ttc cct gat ttc atc cac act caa aaa cga 786
Ile Arg Asp Ala Ile Lys Phe Pro Asp Phe Ile His Thr Gln Lys Arg
          140                145                150

gat cct caa acc aat ttg cct aac cat gac atg gta tgg gat ttt tgg 834
Asp Pro Gln Thr Asn Leu Pro Asn His Asp Met Val Trp Asp Phe Trp
          155                160                165

agt aat gtt cct gaa agc tta tac caa gta aca tgg gtt atg agc gat 882
Ser Asn Val Pro Glu Ser Leu Tyr Gln Val Thr Trp Val Met Ser Asp
          170                175                180

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aga ggg att cct aaa tct ttc cgc cac atg gat ggt ttt ggc agt cac 930
Arg Gly Ile Pro Lys Ser Phe Arg His Met Asp Gly Phe Gly Ser His
185 190 195

act ttc agt ctt atc aac gct aaa ggc gaa cgc ttt tgg gtg aaa ttc 978
Thr Phe Ser Leu Ile Asn Ala Lys Gly Glu Arg Phe Trp Val Lys Phe
200 205 210 215

cac ttt cac acc atg caa ggc gtt aag cac ttg act aac gaa gaa gcc 1026
His Phe His Thr Met Gln Gly Val Lys His Leu Thr Asn Glu Glu Ala
220 225 230

gca gaa gtc aga aaa tat gat cct gat tcc aat caa agg gat tta ttc 1074
Ala Glu Val Arg Lys Tyr Asp Pro Asp Ser Asn Gln Arg Asp Leu Phe
235 240 245

aat gcg atc gct aga ggg gat ttc cca aaa tgg aaa tta agc gtt caa 1122
Asn Ala Ile Ala Arg Gly Asp Phe Pro Lys Trp Lys Leu Ser Val Gln
250 255 260

gtg atg cca gaa gaa gat gct aag aag tat cga ttc cat ccg ttt gat 1170
Val Met Pro Glu Glu Asp Ala Lys Lys Tyr Arg Phe His Pro Phe Asp
265 270 275

gtg act aaa att tgg tac ctc caa gat tat ccg ttg atg gaa gtg ggc 1218
Val Thr Lys Ile Trp Tyr Leu Gln Asp Tyr Pro Leu Met Glu Val Gly
280 285 290 295

att gta gag ttg aat aaa aat ccc gaa aac tat ttc gca gaa gtg gag 1266
Ile Val Glu Leu Asn Lys Asn Pro Glu Asn Tyr Phe Ala Glu Val Glu
300 305 310

caa gcg gca ttc agt ccg gct aat gtc gtt cct gga att ggc tat agc 1314
Gln Ala Ala Phe Ser Pro Ala Asn Val Val Pro Gly Ile Gly Tyr Ser
315 320 325

cct gat agg atg tta caa ggg cgc ttg ttc tct tat ggg gat aca cac 1362
Pro Asp Arg Met Leu Gln Gly Arg Leu Phe Ser Tyr Gly Asp Thr His
330 335 340

cgc tac cgc tta ggg gtt aat tac cct caa ata ccg gtt aat aaa cca 1410
Arg Tyr Arg Leu Gly Val Asn Tyr Pro Gln Ile Pro Val Asn Lys Pro
345 350 355

aga tgc ccg ttc cac tct tct agc aga gat ggt tac atg caa aat ggg 1458
Arg Cys Pro Phe His Ser Ser Ser Arg Asp Gly Tyr Met Gln Asn Gly
360 365 370 375

tat tac ggc tct tta caa aac tat acg cct agc tca ttg cct ggc tat 1506
Tyr Tyr Gly Ser Leu Gln Asn Tyr Thr Pro Ser Ser Leu Pro Gly Tyr
380 385 390

aaa gaa gat aag agc gcg aga gat cct aaa ttc aac tta gct cat att 1554
Lys Glu Asp Lys Ser Ala Arg Asp Pro Lys Phe Asn Leu Ala His Ile
395 400 405

gag aaa gag ttt gaa gtg tgg aat tgg gat tac aga gct gat gat agc 1602
Glu Lys Glu Phe Glu Val Trp Asn Trp Asp Tyr Arg Ala Asp Asp Ser
410 415 420

gat tac tac acc caa cca ggt gat tac tac cgc tca ttg cca gct gat 1650
Asp Tyr Tyr Thr Gln Pro Gly Asp Tyr Tyr Arg Ser Leu Pro Ala Asp
425 430 435

gaa aaa gaa agg ttg cat gac act att gga gag tct ttg gct cat gtt 1698
Glu Lys Glu Arg Leu His Asp Thr Ile Gly Glu Ser Leu Ala His Val
440 445 450 455

acc cat aag gaa att gtg gat aaa caa ttg gag cat ttc aag aaa gct 1746
Thr His Lys Glu Ile Val Asp Lys Gln Leu Glu His Phe Lys Lys Ala

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460

465

470

gac ccc aaa tac gct gag ggg gtt aaa aaa gct ctt gaa aaa cac caa 1794
 Asp Pro Lys Tyr Ala Glu Gly Val Lys Lys Ala Leu Glu Lys His Gln
 475 480 485

aaa atg atg aaa gac atg cat gga aaa gac atg cac cac aca aaa aag 1842
 Lys Met Met Lys Asp Met His Gly Lys Asp Met His His Thr Lys Lys
 490 495 500

aaa aag taa cccttttctt taagcgttct tatttttttag gaacgctttg 1891
 Lys Lys
 505

tctttcaaaa tttagggtttt tggataactca tcagtcctttt ggtgggtgtgt cctattttttt 1951

cattcattca acgaatttaa aaattacaat aaagagttat agttatgaaa cgaagggatt 2011

ttattaaaac gactgcttta ggcgctacag gtgctgtttt aggagcacag attttgacagg 2071

cagaagaaaag caaagggagt gttgcaaaat ataaaataga agctcaatac agcattgatt 2131

ttgattctgc agaacacact tcgcttttca ttcccatgcc gagtgttgta gcgagcaatg 2191

tgcatattaca aggcaatcat gccagctata aaagcatgct caatttttga gtgccttatt 2251

tgcaagtgga ttttttaaaa agcgcctcaaa aaaagcaagt ccatttgtct tatgagatc 2310

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<212> PRT

<213> Helicobacter pylori

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 20 25 30
 Leu Gln Ser Thr Trp Phe Leu Glu Lys Leu Ala Ala Phe Asp Arg Glu
 35 40 45
 Arg Ile Pro Glu Arg Val Val His Ala Lys Gly Ser Gly Ala Tyr Gly
 50 55 60
 Thr Phe Thr Val Thr Lys Asp Ile Thr Lys Tyr Thr Lys Ala Lys Ile
 65 70 75 80
 Phe Ser Lys Val Gly Lys Lys Thr Glu Cys Phe Phe Arg Phe Ser Thr
 85 90 95
 Val Ala Gly Glu Arg Gly Ser Ala Asp Ala Val Arg Asp Pro Arg Gly
 100 105 110
 Phe Ala Met Lys Tyr Tyr Thr Glu Gly Asn Trp Asp Leu Val Gly
 115 120 125
 Asn Asn Thr Pro Val Phe Phe Ile Arg Asp Ala Ile Lys Phe Pro Asp
 130 135 140
 Phe Ile His Thr Gln Lys Arg Asp Pro Gln Thr Asn Leu Pro Asn His
 145 150 155 160
 Asp Met Val Trp Asp Phe Trp Ser Asn Val Pro Glu Ser Leu Tyr Gln
 165 170 175
 Val Thr Trp Val Met Ser Asp Arg Gly Ile Pro Lys Ser Phe Arg His
 180 185 190
 Met Asp Gly Phe Gly Ser His Thr Phe Ser Leu Ile Asn Ala Lys Gly
 195 200 205
 Glu Arg Phe Trp Val Lys Phe His Phe His Thr Met Gln Gly Val Lys
 210 215 220
 His Leu Thr Asn Glu Glu Ala Ala Glu Val Arg Lys Tyr Asp Pro Asp
 225 230 235 240
 Ser Asn Gln Arg Asp Leu Phe Asn Ala Ile Ala Arg Gly Asp Phe Pro
 245 250 255
 Lys Trp Lys Leu Ser Val Gln Val Met Pro Glu Glu Asp Ala Lys Lys
 260 265 270

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Tyr Arg Phe His Pro Phe Asp Val Thr Lys Ile Trp Tyr Leu Gln Asp
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Tyr Pro Leu Met Glu Val Gly Ile Val Glu Leu Asn Lys Asn Pro Glu
      290      295      300
Asn Tyr Phe Ala Glu Val Glu Gln Ala Ala Phe Ser Pro Ala Asn Val
      305      310      315
Val Pro Gly Ile Gly Tyr Ser Pro Asp Arg Met Leu Gln Gly Arg Leu
      325      330      335
Phe Ser Tyr Gly Asp Thr His Arg Tyr Arg Leu Gly Val Asn Tyr Pro
      340      345      350
Gln Ile Pro Val Asn Lys Pro Arg Cys Pro Phe His Ser Ser Ser Arg
      355      360      365
Asp Gly Tyr Met Gln Asn Gly Tyr Tyr Gly Ser Leu Gln Asn Tyr Thr
      370      375      380
Pro Ser Ser Leu Pro Gly Tyr Lys Glu Asp Lys Ser Ala Arg Asp Pro
      385      390      395
Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu Val Trp Asn Trp
      405      410      415
Asp Tyr Arg Ala Asp Asp Ser Asp Tyr Tyr Thr Gln Pro Gly Asp Tyr
      420      425      430
Tyr Arg Ser Leu Pro Ala Asp Glu Lys Glu Arg Leu His Asp Thr Ile
      435      440      445
Gly Glu Ser Leu Ala His Val Thr His Lys Glu Ile Val Asp Lys Gln
      450      455      460
Leu Glu His Phe Lys Lys Ala Asp Pro Lys Tyr Ala Glu Gly Val Lys
      465      470      475
Lys Ala Leu Glu Lys His Gln Lys Met Met Lys Asp Met His Gly Lys
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Asp Met His His Thr Lys Lys Lys Lys
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<210> 22

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<400> 22

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  1              5              10              15

gtg gat gtg ggg aaa gaa caa atc ggt att act gat agc atg ctc ttg      96
Val Asp Val Gly Lys Glu Gln Ile Gly Ile Thr Asp Ser Met Leu Leu
      20              25              30

gtg gct caa aac atc gtt tta gct tta ggg caa gtg gat ttg agc aaa      144
Val Ala Gln Asn Ile Val Leu Ala Leu Gly Gln Val Asp Leu Ser Lys
      35              40              45

atc caa caa aat aaa aat aat ggt aac gga cag cta tac gaa aac atc      192
Ile Gln Gln Asn Lys Asn Asn Gly Asn Gly Gln Leu Tyr Glu Asn Ile
      50              55              60

atg aaa gtc atg ctt tta ggt gcg ggc ggg act aat gga gcg tat aat      240
Met Lys Val Met Leu Leu Gly Ala Gly Gly Thr Asn Gly Ala Tyr Asn
      65              70              75

ggc gtg agt gtg ggc gat att gcc aca ggc atg caa aat ttt tct tcg      288
Gly Val Ser Val Gly Asp Ile Ala Thr Gly Met Gln Asn Phe Ser Ser
      85              90              95

caa acg ggc ttg ata ggg gct aat tct acg gtt agc gag ctc aac gct      336
Gln Thr Gly Leu Ile Gly Ala Asn Ser Thr Val Ser Glu Leu Asn Ala

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ttg att aag agc ggg att tct tta gat cgt gag act ttg agg tta ggg 384
Leu Ile Lys Ser Gly Ile Ser Leu Asp Arg Glu Thr Leu Arg Leu Gly
115          120          125

agt ttt att gaa aaa aat att tgt agc agt gca tcg tct tgt ttt act 432
Ser Phe Ile Glu Lys Asn Ile Cys Ser Ser Ala Ser Ser Cys Phe Thr
130          135          140

ggg agt cag ctt atc tat aag aaa ggg cta gat aga acc ata aac atc 480
Gly Ser Gln Leu Ile Tyr Lys Lys Gly Leu Asp Arg Thr Ile Asn Ile
145          150          155

att aat gcg gta tta ggt cag ttt gaa tct tcg gct agt tct ctt tat 528
Ile Asn Ala Val Leu Gly Gln Phe Glu Ser Ser Ala Ser Ser Leu Tyr
165          170          175

aag att tct tat atc cct aac ctc ttt tcg ctc aaa gat tac cag tca 576
Lys Ile Ser Tyr Ile Pro Asn Leu Phe Ser Leu Lys Asp Tyr Gln Ser
180          185          190

gcg agc atg aac ggc ttt ggg gct aag atg ggt tat aaa caa ttt ttc 624
Ala Ser Met Asn Gly Phe Gly Ala Lys Met Gly Tyr Lys Gln Phe Phe
195          200          205

acc cat aag aaa aat att ggc tta agg tat tac ggg ttt ttg gat tat 672
Thr His Lys Lys Asn Ile Gly Leu Arg Tyr Tyr Gly Phe Leu Asp Tyr
210          215          220

ggc tat gcg aat ttt ggc gat acg aat tta aaa gtg gga gcg aat ctt 720
Gly Tyr Ala Asn Phe Gly Asp Thr Asn Leu Lys Val Gly Ala Asn Leu
225          230          235

gtt act tat ggg gta gga acg gat ttt tta tac aac gtg tat gaa cgc 768
Val Thr Tyr Gly Val Gly Thr Asp Phe Leu Tyr Asn Val Tyr Glu Arg
245          250          255

tct aga agg agg gaa agg act aca atc ggc ctt ttc ttt ggc gct caa 816
Ser Arg Arg Arg Glu Arg Thr Thr Ile Gly Leu Phe Phe Gly Ala Gln
260          265          270

att gca ggg caa act tgg agc act aat gta acg aac tta ttg agc ggg 864
Ile Ala Gly Gln Thr Trp Ser Thr Asn Val Thr Asn Leu Leu Ser Gly
275          280          285

caa agg cct gat gtc aag tct agt tcg ttc caa ttc ttg ttt gat ttg 912
Gln Arg Pro Asp Val Lys Ser Ser Ser Phe Gln Phe Leu Phe Asp Leu
290          295          300

ggc gtg cgc acc aac ttt gca aaa acc aat ttc aac aag cac agg cta 960
Gly Val Arg Thr Asn Phe Ala Lys Thr Asn Phe Asn Lys His Arg Leu
305          310          315

gac caa ggg ata gaa ttt ggg gtg aaa atc cct gtt atc gct cat aaa 1008
Asp Gln Gly Ile Glu Phe Gly Val Lys Ile Pro Val Ile Ala His Lys
325          330          335

tat ttc gca acc caa ggc tca agc gcg agc tat atg agg aat ttt agc 1056
Tyr Phe Ala Thr Gln Gly Ser Ser Ala Ser Tyr Met Arg Asn Phe Ser
340          345          350

ttc tat gtg ggc tat tca gtc ggt ttt taa ggaaggctct tgatgaaaaa 1106
Phe Tyr Val Gly Tyr Ser Val Gly Phe
355          360

taccaataca aaagagataa agaatacaag aatgaaaaaa gggttatagtc aataccatgc 1166
gctcaaaaaa gggctttttaaa aaactgctct gcttttttagc cttcccttaa gcatggcggtt 1226

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CHIR0340.ST25.txt

agctgaagac gatggctttt atatgggagt gggctatcaa atcggcgggtg cgcaacaaaa 1286
 catcaataac aaaggcagca ccctaaggaa taatgtcatt gatgatttcc gccaaagtggg 1346
 cgtgggtatg gcagggggta acgggctttt agctttagcg acaaacacga ccatggacgc 1406
 tcttttaggg ataggcaacc aaattgtcaa taccaatata actgttggca acaacaacgc 1466
 agagttaacc cagtttaaaa aaatactccc ccaaattgag cgacgctttg agacgaataa 1526
 aaacgcttat agcgttcaag ccttgcaagt gtatttgagt aatgtgcttt ataacttggg 1586
 taataatagt aataatggca gtaataatgg agtcgttctt gaatatgtag ggattataaa 1646
 agttctctat aattctcaaa atgaattcag tctcttagcc acggagagtg tggcgctttt 1706
 aaacgcgctt acaaggggtga atctggatag caattcgggtg tttttaaaag ggctattagc 1766
 ccaaatgcag ctttttaatg acacttcttc agcaaagcta ggccagatcg cagaaaactt 1826
 gaataagagt ggtgggtgcag gggccatgct tcaaaaggat gtgaaaacca tctcggatcg 1886
 aatcgctact taccaagaga atctaaaaca actaggaggg atgctgaata attacgatga 1946
 gccttacttg cccaatttg ggccaggcaa aagctctcag catgggggtta ttaatggctt 2006
 tggcattcaa gtgggctata agcaattttt tgggagcaag aggaatatag gcttacggta 2066
 ttacgccttc tttgattatg gctttacgca attgggcagt cttaatagcg ctgttaaagc 2126
 gaacatcttt acttatggcg ctggcacgga ctttttatgg aatatcttta gaagggtttt 2186
 tagcgatcag tctttgaatg tgggggtggt tgggggcatt caaatagcgg gtaacacttg 2246
 ggatagctct ttaagaggcc aaattgaaaa ctctgtttaa gaatacccca ctcccacgaa 2306
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 gtttttgagc tcgtctcaaa gcattcagca tggatggaa tttggcgtga aaatcccggc 2426
 tatcaatcaa aggtatttga aagcgaatgg ggctgatgtg gattacaggc gtttgtatgc 2486
 gtcttatatc aactacacga taggttttta agctcttttt agggcttata aagaggttct 2546
 ttactttttt ttggtattct aacaagcttt taaaccatcc aatctacttt gttttaagga 2606
 taatatttta tggcagatgt cgttgtgggg atc 2639

<210> 23

<211> 361

<212> PRT

<213> *Helicobacter pylori*

<400> 23

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			20					25					30		
Val	Ala	Gln	Asn	Ile	Val	Leu	Ala	Leu	Gly	Gln	Val	Asp	Leu	Ser	Lys
		35					40					45			
Ile	Gln	Gln	Asn	Lys	Asn	Asn	Gly	Asn	Gly	Gln	Leu	Tyr	Glu	Asn	Ile
	50				55					60					
Met	Lys	Val	Met	Leu	Leu	Gly	Ala	Gly	Gly	Thr	Asn	Gly	Ala	Tyr	Asn
	65			70					75					80	
Gly	Val	Ser	Val	Gly	Asp	Ile	Ala	Thr	Gly	Met	Gln	Asn	Phe	Ser	Ser
			85					90					95		
Gln	Thr	Gly	Leu	Ile	Gly	Ala	Asn	Ser	Thr	Val	Ser	Glu	Leu	Asn	Ala
		100					105					110			
Leu	Ile	Lys	Ser	Gly	Ile	Ser	Leu	Asp	Arg	Glu	Thr	Leu	Arg	Leu	Gly

CHIR0340.ST25.txt

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      115      120      125
Ser Phe Ile Glu Lys Asn Ile Cys Ser Ser Ala Ser Ser Cys Phe Thr
      130      135      140
Gly Ser Gln Leu Ile Tyr Lys Lys Gly Leu Asp Arg Thr Ile Asn Ile
145      150      155      160
Ile Asn Ala Val Leu Gly Gln Phe Glu Ser Ser Ala Ser Ser Leu Tyr
      165      170      175
Lys Ile Ser Tyr Ile Pro Asn Leu Phe Ser Leu Lys Asp Tyr Gln Ser
      180      185      190
Ala Ser Met Asn Gly Phe Gly Ala Lys Met Gly Tyr Lys Gln Phe Phe
      195      200      205
Thr His Lys Lys Asn Ile Gly Leu Arg Tyr Tyr Gly Phe Leu Asp Tyr
      210      215      220
Gly Tyr Ala Asn Phe Gly Asp Thr Asn Leu Lys Val Gly Ala Asn Leu
225      230      235      240
Val Thr Tyr Gly Val Gly Thr Asp Phe Leu Tyr Asn Val Tyr Glu Arg
      245      250      255
Ser Arg Arg Arg Glu Arg Thr Thr Ile Gly Leu Phe Phe Gly Ala Gln
      260      265      270
Ile Ala Gly Gln Thr Trp Ser Thr Asn Val Thr Asn Leu Leu Ser Gly
      275      280      285
Gln Arg Pro Asp Val Lys Ser Ser Ser Phe Gln Phe Leu Phe Asp Leu
290      295      300
Gly Val Arg Thr Asn Phe Ala Lys Thr Asn Phe Asn Lys His Arg Leu
305      310      315      320
Asp Gln Gly Ile Glu Phe Gly Val Lys Ile Pro Val Ile Ala His Lys
      325      330      335
Tyr Phe Ala Thr Gln Gly Ser Ser Ala Ser Tyr Met Arg Asn Phe Ser
      340      345      350
Phe Tyr Val Gly Tyr Ser Val Gly Phe
      355      360

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<210> 24
 <211> 2639
 <212> DNA
 <213> *Helicobacter pylori*

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 <222> (1099)..(2517)
 <223> signal peptide of protein

<220>
 <221> mat_peptide
 <222> (1231)
 <223> mature protein HopX

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ttagggcaag tggatttgag caaatccaa caaataaaaa ataatggtaa cggacagcta 180
tacgaaaaca tcatgaaagt catgctttta ggtgcgggcg ggactaatgg agcgtataat 240
ggcgtgagtg tgggcgatat tgccacaggc atgcaaaatt tttcttcgca aacgggcttg 300
ataggggcta attctacggt tagcgagctc aacgctttga ttaagagcgg gatttcttta 360
gatcgtgaga ctttgagggt agggagtttt attgaaaaaa atattttagt cagtgcacgc 420
tcttggttta ctgggagtca gcttatctat aagaaagggc tagatagaac cataaacatc 480
attaatgcgg tattaggtca gtttgaatct tcggctagtt ctctttataa gatttcttat 540
atccctaacc tcttttcgct caaagattac cagtcagcga gcatgaacgg ctttggggct 600

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aagatggggtt ataaacaatt tttcacccat aagaaaaata ttggcttaag gtattacggg 660
tttttggatt atggctatgc gaattttggc gatacgaatt taaaagtggg agcgaatctt 720
gttacttatg gggtaggaac ggatttttta tacaacgtgt atgaacgctc tagaaggagg 780
gaaaggacta caatcggcct tttctttggc gctcaaattg cagggcaaac ttggagcact 840
aatgtaacga acttattgag cgggcaaagg cctgatgtca agtctagttc gttccaattc 900
ttgtttgatt tgggcgtgcg caccaacttt gcaaaaacca atttcaacaa gcacaggcta 960
gaccaaggga tagaatttgg ggtgaaaatc cctgttatcg ctcataaata tttcgcaacc 1020
caaggctcaa gcgcgagcta tatgaggaat tttagcttct atgtgggcta ttcagtcggt 1080

ttttaaggaa ggctcttg atg aaa aat acc aat aca aaa gag ata aag aat 1131
Met Lys Asn Thr Asn Thr Lys Glu Ile Lys Asn
-40 -35

aca aga atg aaa aaa ggt tat agt caa tac cat gcg ctc aaa aaa ggg 1179
Thr Arg Met Lys Lys Gly Tyr Ser Gln Tyr His Ala Leu Lys Lys Gly
-30 -25 -20

ctt tta aaa act gct ctg ctt ttt agc ctt ccc tta agc atg gcg tta 1227
Leu Leu Lys Thr Ala Leu Leu Phe Ser Leu Pro Leu Ser Met Ala Leu
-15 -10 -5

gct gaa gac gat ggc ttt tat atg gga gtg ggc tat caa atc ggc ggt 1275
Ala Glu Asp Asp Gly Phe Tyr Met Gly Val Gly Tyr Gln Ile Gly Gly
-1 1 5 10 15

gcg caa caa aac atc aat aac aaa ggc agc acc cta agg aat aat gtc 1323
Ala Gln Gln Asn Ile Asn Asn Lys Gly Ser Thr Leu Arg Asn Asn Val
20 25 30

att gat gat ttc cgc caa gtg ggc gtg ggt atg gca ggg ggt aac ggg 1371
Ile Asp Asp Phe Arg Gln Val Gly Val Gly Met Ala Gly Gly Asn Gly
35 40 45

ctt tta gct tta gcg aca aac acg acc atg gac gct ctt tta ggg ata 1419
Leu Leu Ala Leu Ala Thr Asn Thr Thr Met Asp Ala Leu Leu Gly Ile
50 55 60

ggc aac caa att gtc aat acc aat aca act gtt ggc aac aac aac gca 1467
Gly Asn Gln Ile Val Asn Thr Asn Thr Thr Val Gly Asn Asn Asn Ala
65 70 75

gag tta acc cag ttt aaa aaa ata ctc ccc caa att gag cga cgc ttt 1515
Glu Leu Thr Gln Phe Lys Lys Ile Leu Pro Gln Ile Glu Arg Arg Phe
80 85 90 95

gag acg aat aaa aac gct tat agc gtt caa gcc ttg caa gtg tat ttg 1563
Glu Thr Asn Lys Asn Ala Tyr Ser Val Gln Ala Leu Gln Val Tyr Leu
100 105 110

agt aat gtg ctt tat aac ttg gtt aat aat agt aat aat ggc agt aat 1611
Ser Asn Val Leu Tyr Asn Leu Val Asn Asn Ser Asn Asn Gly Ser Asn
115 120 125

aat gga gtc gtt cct gaa tat gta ggg att ata aaa gtt ctc tat aat 1659
Asn Gly Val Val Pro Glu Tyr Val Gly Ile Ile Lys Val Leu Tyr Asn
130 135 140

tct caa aat gaa ttc agt ctc tta gcc acg gag agt gtg gcg ctt tta 1707
Ser Gln Asn Glu Phe Ser Leu Leu Ala Thr Glu Ser Val Ala Leu Leu
145 150 155

aac gcg ctt aca agg gtg aat ctg gat agc aat tcg gtg ttt tta aaa 1755
Asn Ala Leu Thr Arg Val Asn Leu Asp Ser Asn Ser Val Phe Leu Lys

CHIR0340.ST25.txt

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160              165              170              175
ggg cta tta gcc caa atg cag ctt ttt aat gac act tct tca gca aag 1803
Gly Leu Leu Ala Gln Met Gln Leu Phe Asn Asp Thr Ser Ser Ala Lys
180              185              190

cta ggc cag atc gca gaa aac ttg aat aag agt ggt ggt gca ggg gcc 1851
Leu Gly Gln Ile Ala Glu Asn Leu Asn Lys Ser Gly Gly Ala Gly Ala
195              200              205

atg ctt caa aag gat gtg aaa acc atc tcg gat cga atc gct act tac 1899
Met Leu Gln Lys Asp Val Lys Thr Ile Ser Asp Arg Ile Ala Thr Tyr
210              215              220

caa gag aat cta aaa caa cta gga ggg atg ctg aat aat tac gat gag 1947
Gln Glu Asn Leu Lys Gln Leu Gly Gly Met Leu Asn Asn Tyr Asp Glu
225              230              235

cct tac ttg ccc caa ttt ggg cca ggc aaa agc tct cag cat ggg gtt 1995
Pro Tyr Leu Pro Gln Phe Gly Pro Gly Lys Ser Ser Gln His Gly Val
240              245              250

att aat ggc ttt ggc att caa gtg ggc tat aag caa ttt ttt ggg agc 2043
Ile Asn Gly Phe Gly Ile Gln Val Gly Tyr Lys Gln Phe Phe Gly Ser
260              265              270

aag agg aat ata ggc tta cgg tat tac gct ttc ttt gat tat ggc ttt 2091
Lys Arg Asn Ile Gly Leu Arg Tyr Tyr Ala Phe Phe Asp Tyr Gly Phe
275              280              285

acg caa ttg ggc agt ctt aat agc gct gtt aaa gcg aac atc ttt act 2139
Thr Gln Leu Gly Ser Leu Asn Ser Ala Val Lys Ala Asn Ile Phe Thr
290              295              300

tat ggc gct ggc acg gac ttt tta tgg aat atc ttt aga agg gtt ttt 2187
Tyr Gly Ala Gly Thr Asp Phe Leu Trp Asn Ile Phe Arg Arg Val Phe
305              310              315

agc gat cag tct ttg aat gtg ggg gtg ttt ggg ggc att caa ata gcg 2235
Ser Asp Gln Ser Leu Asn Val Gly Val Phe Gly Gly Ile Gln Ile Ala
320              325              335

ggt aac act tgg gat agc tct tta aga ggc caa att gaa aac tcg ttt 2283
Gly Asn Thr Trp Asp Ser Ser Leu Arg Gly Gln Ile Glu Asn Ser Phe
340              345              350

aaa gaa tac ccc act ccc acg aat ttc caa ttt tta ttt aat ttg ggc 2331
Lys Glu Tyr Pro Thr Pro Thr Asn Phe Gln Phe Leu Phe Asn Leu Gly
355              360              365

tta agg gct cat ttt gcc agc acc atg cac cgc cgg ttt ttg agc tcg 2379
Leu Arg Ala His Phe Ala Ser Thr Met His Arg Arg Phe Leu Ser Ser
370              375              380

tct caa agc att cag cat ggt atg gaa ttt ggc gtg aaa atc ccg gct 2427
Ser Gln Ser Ile Gln His Gly Met Glu Phe Gly Val Lys Ile Pro Ala
385              390              395

atc aat caa agg tat ttg aaa gcg aat ggg gct gat gtg gat tac agg 2475
Ile Asn Gln Arg Tyr Leu Lys Ala Asn Gly Ala Asp Val Asp Tyr Arg
400              405              410

cgt ttg tat gcg ttc tat atc aac tac acg ata ggt ttt taa 2517
Arg Leu Tyr Ala Phe Tyr Ile Asn Tyr Thr Ile Gly Phe
420              425

gctcttttta gggcttataa agaggttctt tacttttttt tggtattota acaagctttt 2577
aaaccatcca atctactttg ttttaaggat aatatatttat ggcagatgtc gttgtgggga 2637

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tc

2639

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 <211> 472
 <212> PRT
 <213> *Helicobacter pylori*

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 20 25 30
 Leu Leu Phe Ser Leu Pro Leu Ser Met Ala Leu Ala Glu Asp Asp Gly
 35 40 45
 Phe Tyr Met Gly Val Gly Tyr Gln Ile Gly Gly Ala Gln Gln Asn Ile
 50 55 60
 Asn Asn Lys Gly Ser Thr Leu Arg Asn Asn Val Ile Asp Asp Phe Arg
 65 70 75 80
 Gln Val Gly Val Gly Met Ala Gly Gly Asn Gly Leu Leu Ala Leu Ala
 85 90 95
 Thr Asn Thr Thr Met Asp Ala Leu Leu Gly Ile Gly Asn Gln Ile Val
 100 105 110
 Asn Thr Asn Thr Thr Val Gly Asn Asn Asn Ala Glu Leu Thr Gln Phe
 115 120 125
 Lys Lys Ile Leu Pro Gln Ile Glu Arg Arg Phe Glu Thr Asn Lys Asn
 130 135 140
 Ala Tyr Ser Val Gln Ala Leu Gln Val Tyr Leu Ser Asn Val Leu Tyr
 145 150 155 160
 Asn Leu Val Asn Asn Ser Asn Asn Gly Ser Asn Asn Gly Val Val Pro
 165 170 175
 Glu Tyr Val Gly Ile Ile Lys Val Leu Tyr Asn Ser Gln Asn Glu Phe
 180 185 190
 Ser Leu Leu Ala Thr Glu Ser Val Ala Leu Leu Asn Ala Leu Thr Arg
 195 200 205
 Val Asn Leu Asp Ser Asn Ser Val Phe Leu Lys Gly Leu Leu Ala Gln
 210 215 220
 Met Gln Leu Phe Asn Asp Thr Ser Ser Ala Lys Leu Gly Gln Ile Ala
 225 230 235 240
 Glu Asn Leu Asn Lys Ser Gly Gly Ala Gly Ala Met Leu Gln Lys Asp
 245 250 255
 Val Lys Thr Ile Ser Asp Arg Ile Ala Thr Tyr Gln Glu Asn Leu Lys
 260 265 270
 Gln Leu Gly Gly Met Leu Asn Asn Tyr Asp Glu Pro Tyr Leu Pro Gln
 275 280 285
 Phe Gly Pro Gly Lys Ser Ser Gln His Gly Val Ile Asn Gly Phe Gly
 290 295 300
 Ile Gln Val Gly Tyr Lys Gln Phe Phe Gly Ser Lys Arg Asn Ile Gly
 305 310 315 320
 Leu Arg Tyr Tyr Ala Phe Phe Asp Tyr Gly Phe Thr Gln Leu Gly Ser
 325 330 335
 Leu Asn Ser Ala Val Lys Ala Asn Ile Phe Thr Tyr Gly Ala Gly Thr
 340 345 350
 Asp Phe Leu Trp Asn Ile Phe Arg Arg Val Phe Ser Asp Gln Ser Leu
 355 360 365
 Asn Val Gly Val Phe Gly Gly Ile Gln Ile Ala Gly Asn Thr Trp Asp
 370 375 380
 Ser Ser Leu Arg Gly Gln Ile Glu Asn Ser Phe Lys Glu Tyr Pro Thr
 385 390 395 400
 Pro Thr Asn Phe Gln Phe Leu Phe Asn Leu Gly Leu Arg Ala His Phe
 405 410 415
 Ala Ser Thr Met His Arg Arg Phe Leu Ser Ser Ser Gln Ser Ile Gln
 420 425 430
 His Gly Met Glu Phe Gly Val Lys Ile Pro Ala Ile Asn Gln Arg Tyr
 435 440 445
 Leu Lys Ala Asn Gly Ala Asp Val Asp Tyr Arg Arg Leu Tyr Ala Phe
 450 455 460
 Tyr Ile Asn Tyr Thr Ile Gly Phe
 465 470

<210> 26
 <211> 1710
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (1)..(1179)
 <223> mature peptide (without N-Terminus); protein HopZ
 of Helicobacter pylori

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 1 5 10 15
 ccg caa aac aat caa aac gcg ccg caa gat ttc aat cct tac acc tct 96
 Pro Gln Asn Asn Gln Asn Ala Pro Gln Asp Phe Asn Pro Tyr Thr Ser
 20 25 30
 gct gat agg gct ttc gct caa aac atg ctc aat cac gcg caa gcg caa 144
 Ala Asp Arg Ala Phe Ala Gln Asn Met Leu Asn His Ala Gln Ala Gln
 35 40 45
 gcc aag atg ctt gaa cta gcc aat caa atc aaa acc aat ctt agc gct 192
 Ala Lys Met Leu Glu Leu Ala Asn Gln Ile Lys Thr Asn Leu Ser Ala
 50 55 60
 atc ccg caa cat ttc acc aaa gat tac ttg gca gct tgc cgc aat ggg 240
 Ile Pro Gln His Phe Thr Lys Asp Tyr Leu Ala Ala Cys Arg Asn Gly
 65 70 75 80
 ggt ggg aca tta cct gat gca ggg gtt act aac aac act tgg gga gcc 288
 Gly Gly Thr Leu Pro Asp Ala Gly Val Thr Asn Asn Thr Trp Gly Ala
 85 90 95
 ggt tgc gcc tat gtg gaa gag acc ata acg gct tta aac aac agc ctt 336
 Gly Cys Ala Tyr Val Glu Glu Thr Ile Thr Ala Leu Asn Asn Ser Leu
 100 105 110
 gtg cat ttt ggc act caa gcc gag caa atc aag caa tct gag ttg ctg 384
 Val His Phe Gly Thr Gln Ala Glu Gln Ile Lys Gln Ser Glu Leu Leu
 115 120 125
 gcg cgc acg ata ttt gat ttt aaa ggc agc ctt aag gat tta aac agc 432
 Ala Arg Thr Ile Phe Asp Phe Lys Gly Ser Leu Lys Asp Leu Asn Ser
 130 135 140
 act tat aac agc atc acc acg acc gct tca aac acg ccc aat tcc cca 480
 Thr Tyr Asn Ser Ile Thr Thr Thr Ala Ser Asn Thr Pro Asn Ser Pro
 145 150 155 160
 ttc ctt aaa aat ttg ata agc caa tcc act aac cct aat aac ccc ggg 528
 Phe Leu Lys Asn Leu Ile Ser Gln Ser Thr Asn Pro Asn Asn Pro Gly
 165 170 175
 ggc tta cag gcc gtt tat caa gtc aac caa agc gct tat tcg caa tta 576
 Gly Leu Gln Ala Val Tyr Gln Val Asn Gln Ser Ala Tyr Ser Gln Leu
 180 185 190
 tta agc gcc acg caa gaa tta ggg cat aac cct ttc aga cgc ttt gga 624
 Leu Ser Ala Thr Gln Glu Leu Gly His Asn Pro Phe Arg Arg Phe Gly
 195 200 205
 tta atc agc tct caa acc aac aat ggt gcc atg aat ggg atc ggt gtg 672
 Leu Ile Ser Ser Gln Thr Asn Asn Gly Ala Met Asn Gly Ile Gly Val
 210 215 220

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caa ata ggg tat aaa caa ttt ttt ggt gaa aag aga aaa tgg ggg gct	720
Gln Ile Gly Tyr Lys Gln Phe Phe Gly Glu Lys Arg Lys Trp Gly Ala	
225 230 235 240	
agg tat tac ggc ttt ttt gac tat aac cat gct tat atc aaa tcc agc	768
Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn His Ala Tyr Ile Lys Ser Ser	
245 250 255	
ttt ttc aac tcc gcc tct gat gtg ttc act tat ggg gta gga aca gat	816
Phe Phe Asn Ser Ala Ser Asp Val Phe Thr Tyr Gly Val Gly Thr Asp	
260 265 270	
gtc ctc tat aac ttt atc aac gat aaa gcc acc aaa aac aat aag att	864
Val Leu Tyr Asn Phe Ile Asn Asp Lys Ala Thr Lys Asn Asn Lys Ile	
275 280 285	
tct ttt ggg gtg ttt ggg ggg att gct tta gct ggc act tcg tgg ctc	912
Ser Phe Gly Val Phe Gly Gly Ile Ala Leu Ala Gly Thr Ser Trp Leu	
290 295 300	
aat tct caa tac gtg aat tta gcg acc ttc aat aat ttc tat agc gct	960
Asn Ser Gln Tyr Val Ala Asn Leu Ala Thr Phe Asn Asn Phe Tyr Ser Ala	
305 310 315 320	
aaa atg aat gtg gcg aat ttc caa ttc tta ttc aac ttg ggc ttg aga	1008
Lys Met Asn Val Ala Asn Phe Gln Phe Leu Phe Asn Leu Gly Leu Arg	
325 330 335	
atg aat ctg gct aaa aac aaa aag aaa gcg agc gat cat gcg gct caa	1056
Met Asn Leu Ala Lys Asn Lys Lys Lys Ala Ser Asp His Ala Ala Gln	
340 345 350	
cat ggc gtg gaa cta ggc gtg aag atc ccc acg atc aac acg aat tac	1104
His Gly Val Glu Leu Gly Val Lys Ile Pro Thr Ile Asn Thr Asn Tyr	
355 360 365	
tat tct ttg cta ggc act caa cta gaa tac cgc aga ctc tat agc gtg	1152
Tyr Ser Leu Leu Gly Thr Gln Leu Glu Tyr Arg Arg Leu Tyr Ser Val	
370 375 380	
tat ttg aat tat gtg ttt gcg tat taa aagcttgctg taaacccttt	1199
Tyr Leu Asn Tyr Val Phe Ala Tyr	
385 390	
gtggaactcc ctttttaagg ggtttctttt gaagcctttt ttttgaacct ttttttgggg	1259
gtcaagcgta aaatccaccc ctatcccttt aagaaaataa aataaaactt taagaacttt	1319
aagaacttta agaaaatgcg ttttacaaca aaataagatc taaaacaata aaacaaaacc	1379
ccatttttta acaatgaaat tttttaaaca aaaaagcatt aaatcctaata aaggtttggt	1439
agatcttgat aaaaacaaag ctttttttaa accccaaaaa caataactaac caataaccaa	1499
aacgcactta ttgtgatcct tatagcataa aaccaagttt ttattttaagc aaaagctggt	1559
atgccgtttt aagagcggtt cgtttctatg aaaaccgcaa tatttttcaa ttattcttga	1619
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CHIR0340.ST25.txt

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Pro Gln Asn Asn Gln Asn Ala Pro Gln Asp Phe Asn Pro Tyr Thr Ser			
	20	25	30
Ala Asp Arg Ala Phe Ala Gln Asn Met Leu Asn His Ala Gln Ala Gln			
	35	40	45
Ala Lys Met Leu Glu Leu Ala Asn Gln Ile Lys Thr Asn Leu Ser Ala			
	50	55	60
Ile Pro Gln His Phe Thr Lys Asp Tyr Leu Ala Ala Cys Arg Asn Gly			
	65	70	75
Gly Gly Thr Leu Pro Asp Ala Gly Val Thr Asn Asn Thr Trp Gly Ala			
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Val His Phe Gly Thr Gln Ala Glu Gln Ile Lys Gln Ser Glu Leu Leu			
	115	120	125
Ala Arg Thr Ile Phe Asp Phe Lys Gly Ser Leu Lys Asp Leu Asn Ser			
	130	135	140
Thr Tyr Asn Ser Ile Thr Thr Ala Ser Asn Thr Pro Asn Ser Pro			
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Gln Ile Gly Tyr Lys Gln Phe Phe Gly Glu Lys Arg Lys Trp Gly Ala			
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Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn His Ala Tyr Ile Lys Ser Ser			
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Lys Met Asn Val Ala Asn Phe Gln Phe Leu Phe Asn Leu Gly Leu Arg			
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 pylori

<400> 28

CHIR0340.ST25.txt

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aag aaa aaa tgg ttt ggt gcg cgt tat tat ggg ttt ttt gac tac gcg 896
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CHIR0340.ST25.txt

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<213> *Helicobacter pylori*

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Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Ala Arg Tyr Tyr Gly
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Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile
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Lys Glu Asn Met Val Phe Gly Phe Val Val Gly Ile Gln Leu Ala Gly
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CHIR0340.ST25.txt

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Tyr Gln Leu Phe Gln Gly Phe Tyr Gly Thr Phe Lys Leu Thr Lys Asn	
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Ala Gly Ile Ile Tyr Arg Pro Thr Lys Asn Leu Met Ile His Pro Tyr	
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Val Tyr Leu Ile Pro Met Val Gly Thr Leu Pro Gly Val Lys Val Glu	
245 250 255	

CHIR0340.ST25.txt

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Tyr Val Lys Gly Gly Gly Lys His Gly Lys Phe Ser Trp Ser Val Tyr	
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 Asn Leu Thr Gly Lys Leu Glu Gly Ser Val His Leu Gly Arg Gly Trp
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 Thr Val Asn Leu Gly Gly Val Leu Gly Gly Gln Ala Tyr Asp Gly Thr
 85 90 95
 Lys Tyr Asp Arg Trp Ala Lys Asp Phe Thr Pro Pro Ser Tyr Trp Asp
 100 105 110
 Lys Thr Ser Cys Gly Thr Asp Ser Met Ser Leu Cys Met Asn Ala Thr
 115 120 125
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 Ile Gly Trp Glu Tyr Met Gly Glu Trp Asn Gly Leu Phe Pro Asn Tyr
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 Tyr Pro Ala Asn Ala Tyr Leu Pro Gly Gly Ser Arg Arg Tyr Gln Val
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 Gly Arg Phe Asp Ile Thr Glu Gln Glu Met Asp Trp Ile Tyr Gln
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 325 330 335
 Trp Arg Gly Leu Gln Gly Pro Gly Gly Ala Thr Leu Leu Arg His
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 Ala Gly Ile Asp Asn Ile Thr Asp Ala Asp Ala Phe Thr Glu Tyr Val
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Leu	Glu	Phe	Gln	Ile	Arg	Ala	Gly	Tyr	Asn	Pro	Gly	Thr	Gly	Phe	Leu
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Ser	Ala	Phe	Ala	Gln	Gly	Pro	Gln	Asn	Met	Gly	Gly	Ile	Ala	Lys	Ser
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<223> bp protein; 42 kD protein from Helicobacter pylori
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CHIR0340.ST25.txt

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Phe	Pro	Gly	Asp	Asp	Thr	Pro	Ile	Val	Ala	Gly	Ser	Ala	Leu	Arg	Ala	
		165					170					175				
tta	gag	gaa	gca	aag	gct	ggt	aat	gtg	ggt	gaa	tgg	ggt	gaa	aaa	gtg	1472
Leu	Glu	Glu	Ala	Lys	Ala	Gly	Asn	Val	Gly	Glu	Trp	Gly	Glu	Lys	Val	
	180					185					190					
ctt	aag	ctc	atg	gct	gaa	gtg	gat	gcc	tat	atc	cct	act	cca	gaa	aga	1520
Leu	Lys	Leu	Met	Ala	Glu	Val	Asp	Ala	Tyr	Ile	Pro	Thr	Pro	Glu	Arg	
					200					205					210	
gac	act	gaa	aaa	act	ttc	ttg	atg	ccg	gtt	gaa	gat	gtg	ttc	tct	att	1568
Asp	Thr	Glu	Lys	Thr	Phe	Leu	Met	Pro	Val	Glu	Asp	Val	Phe	Ser	Ile	
				215					220					225		
g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	1616
Ala	Gly	Arg	Gly	Thr	Val	Val	Thr	Gly	Arg	Ile	Glu	Arg	Gly	Val	Val	
			230					235					240			
aaa	gta	ggc	gat	gaa	gtg	gaa	atc	gtt	ggt	atc	aga	gct	aca	caa	aaa	1664
Lys	Val	Gly	Asp	Glu	Val	Glu	Ile	Val	Gly	Ile	Arg	Ala	Thr	Gln	Lys	
		245					250					255				
acg	act	gta	acc	ggt	gtg	gaa	atg	ttt	aga	aaa	gag	cta	gaa	aaa	ggt	1712
Thr	Thr	Val	Thr	Gly	Val	Glu	Met	Phe	Arg	Lys	Glu	Leu	Glu	Lys	Gly	
		260				265					270					
gag	gcc	ggc	gat	aat	gtg	ggc	gtg	ctt	ttg	aga	gga	act	aaa	aaa	gaa	1760
Glu	Ala	Gly	Asp	Asn	Val	Gly	Val	Leu	Leu	Arg	Gly	Thr	Lys	Lys	Glu	
					280					285					290	
gaa	gta	gaa	cg	ggt	atg	gtt	cta	tgc	aaa	cca	ggt	tct	atc	act	ccg	1808
Glu	Val	Glu	Arg	Gly	Met	Val	Leu	Cys	Lys	Pro	Gly	Ser	Ile	Thr	Pro	
				295					300					305		
cac	aag	aaa	ttt	gag	gga	gaa	att	tat	gtc	ctt	tct	aaa	gaa	gaa	ggc	1856
His	Lys	Lys	Phe	Glu	Gly	Glu	Ile	Tyr	Val	Leu	Ser	Lys	Glu	Glu	Gly	
			310					315					320			
ggg	aga	cac	act	cca	ttc	ttc	acc	aat	tac	cg	ccg	caa	ttc	tat	gtg	1904
Gly	Arg	His	Thr	Pro	Phe	Phe	Thr	Asn	Tyr	Arg	Pro	Gln	Phe	Tyr	Val	
		325					330					335				

CHIR0340.ST25.txt

```

cgc acg act gat gtg act ggc tct atc acc ctt cct gaa ggc gta gaa 1952
Arg Thr Thr Asp Val Thr Gly Ser Ile Thr Leu Pro Glu Gly Val Glu
   340               345               350

atg gtt atg cct ggc gat aat gtg aaa atc act gta gag ttg att agc 2000
Met Val Met Pro Gly Asp Asn Val Lys Ile Thr Val Glu Leu Ile Ser
   355               360               365               370

cct gtt gcg tta gag ttg gga act aaa ttt gcg att cgt gaa ggc ggt 2048
Pro Val Ala Leu Glu Leu Gly Thr Lys Phe Ala Ile Arg Glu Gly Gly
           375               380               385

agg acc gtt ggt gct ggt gtt gtg agc aat att att gaa taa 2090
Arg Thr Val Gly Ala Gly Val Val Ser Asn Ile Ile Glu
           390               395               400

tattagcaaa aagagttacc ataaagggtc attatgaaag ttaaaatagg gttgaagtgt 2150

tctgattgtg aagatatcaa ttacagcaca accaagaacg ctaaaactaa cactgaaaaa 2210

ctggagctta agaagttctg cccaaggga aacaaacaca ctcttcataa agaaatcaaa 2270

ttgaagagct agttctttct tttgtgttgt gattgaaaag gaggggaggt taggtcagta 2330

gctccaatgg tagagcgtcg gtctccaaaa ccggttggtg ggggttcgag tccctcctgg 2390

cctgccatct actaatatct tctatcaaat ttttgtttca attggattgt ttttgaattt 2450

tttaatttta gtttaagcta ttttgataa aattgaaaat tcttttaatg tataaatatt 2510

aagtttaagt gagggcgaaa agaaactatg gataaatggc tcatgcaata taaattagct 2570

agagaagagc tttctaaagt gatatttctt attaaggagc agatacgcaa cgcgcttggt 2630

tctgttttgg tgggtggtgag tgctatcacg ctgttttttag ctttggttga tttttctctg 2690

ggggctttta tctctagtgt tctatagggt ggtggcttta aataaggaga ataatgatgg 2750

attggtatgc catacaaaact tattcaggga gcgagcagtc cgtaaagaaa gcgattgaga 2810

atctagcgaa cgatc 2825

```

<210> 33
 <211> 399
 <212> PRT
 <213> Helicobacter pylori

```

<400> 33
Met Ala Lys Glu Lys Phe Asn Arg Thr Lys Pro His Val Asn Ile Gly
 1           5           10           15
Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Ser Ala Ala Ile
           20           25           30
Ser Ala Val Leu Ser Leu Lys Gly Leu Ala Glu Met Lys Asp Tyr Asp
           35           40           45
Asn Ile Asp Asn Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr Ile Ala
           50           55           60
Thr Ser His Ile Glu Tyr Glu Thr Glu Asn Arg His Tyr Ala His Val
           65           70           75           80
Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
           85           90           95
Ala Gln Met Asp Gly Ala Ile Leu Val Val Ser Ala Ala Asp Gly Pro
           100          105          110
Met Pro Gln Thr Arg Glu His Ile Leu Leu Ser Arg Gln Val Gly Val
           115          120          125
Pro His Ile Val Val Phe Leu Asn Lys Gln Asp Met Val Asp Asp Gln
           130          135          140
Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ser Ala
           145          150          155          160

```

CHIR0340.ST25.txt

```

Tyr Glu Phe Pro Gly Asp Asp Thr Pro Ile Val Ala Gly Ser Ala Leu
      165      170      175
Arg Ala Leu Glu Glu Ala Lys Ala Gly Asn Val Gly Glu Trp Gly Glu
      180      185      190
Lys Val Leu Lys Leu Met Ala Glu Val Asp Ala Tyr Ile Pro Thr Pro
      195      200      205
Glu Arg Asp Thr Glu Lys Thr Phe Leu Met Pro Val Glu Asp Val Phe
      210      215      220
Ser Ile Ala Gly Arg Gly Thr Val Val Thr Gly Arg Ile Glu Arg Gly
      225      230      235      240
Val Val Lys Val Gly Asp Glu Val Glu Ile Val Gly Ile Arg Ala Thr
      245      250      255
Gln Lys Thr Thr Val Thr Gly Val Glu Met Phe Arg Lys Glu Leu Glu
      260      265      270
Lys Gly Glu Ala Gly Asp Asn Val Gly Val Leu Leu Arg Gly Thr Lys
      275      280      285
Lys Glu Glu Val Glu Arg Gly Met Val Leu Cys Lys Pro Gly Ser Ile
      290      295      300
Thr Pro His Lys Lys Phe Glu Gly Glu Ile Tyr Val Leu Ser Lys Glu
      305      310      315      320
Glu Gly Gly Arg His Thr Pro Phe Phe Thr Asn Tyr Arg Pro Gln Phe
      325      330      335
Tyr Val Arg Thr Thr Asp Val Thr Gly Ser Ile Thr Leu Pro Glu Gly
      340      345      350
Val Glu Met Val Met Pro Gly Asp Asn Val Lys Ile Thr Val Glu Leu
      355      360      365
Ile Ser Pro Val Ala Leu Glu Leu Gly Thr Lys Phe Ala Ile Arg Glu
      370      375      380
Gly Gly Arg Thr Val Gly Ala Gly Val Val Ser Asn Ile Ile Glu
      385      390      395

```

<210> 34

<211> 2182

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (344)..(1507)

<223> signal peptide; 36/35/32 kD protein from
Helicobacter protein

<220>

<221> mat_peptide

<222> (521)

<223> mature protein; 36/35/32 kD protein from
Helicobacter protein

<400> 34

```

gatcgctcctt tgagtgattc ctgtattcgc tttattggca aactcttcgc caaacatttt 60
cttcacatta gggaaaatta ccccatcaaa aaacaagtag ccaataaaaa taatggcgca 120
caataaatga acaaccaaca cataaggata aatcgcatcc atttaaaatc ctttattcat 180
gggaaaatta aagagttttt aatctactat aaaagggttt tattgtcaag tatcccacta 240
ttatgggaat tttaggggtg gtttttgttt gacttttaag attgcaatta gctataataa 300
aataattaaa aaagtaaacac ttaagcggag accctagaga gtg atg ctc aat ttt 355
                                     Met Leu Asn Phe
atg aca aag aag aaa aat aga atg caa gat tgc aaa atg gtt ggt aaa 403
Met Thr Lys Lys Lys Asn Arg Met Gln Asp Cys Lys Met Val Gly Lys
-55      -50      -45      -40
aat ttt aat cgt aag gaa tct gtt ttg ata gct caa tct tta gaa att 451
Asn Phe Asn Arg Lys Glu Ser Val Leu Ile Ala Gln Ser Leu Glu Ile

```

	-35	-30	-25	
tct aaa aaa ggc tgc gta att tta ggc gct ctt ttg agt tgc tta tgg				499
Ser Lys Lys Gly Ser Val Ile Leu Gly Ala Leu Ser Ser Leu Trp				
	-20	-15	-10	
ctg aca aac ccc tta aat gcc cat gaa aag aat ggc gcg ttt gtg ggg				547
Leu Thr Asn Pro Leu Asn Ala His Glu Lys Asn Gly Ala Phe Val Gly				
	-5	-1	5	
att agc ttg gaa gtg ggt agg gct gat caa aag acc aac gct tat aga				595
Ile Ser Leu Glu Val Gly Arg Ala Asp Gln Lys Thr Asn Ala Tyr Arg				
	10	15	20	25
aac ggc gag ttg ttt caa gtg cct ttt ggc gat gtt tca gcc aat gat				643
Asn Gly Glu Leu Phe Gln Val Pro Phe Gly Asp Val Ser Ala Asn Asp				
	30	35	40	
gat ggc aaa gtc cct aac ggg cag acc ggt ggc tgt cag cca gct tca				691
Asp Gly Lys Val Pro Asn Gly Gln Thr Gly Gly Cys Gln Pro Ala Ser				
	45	50	55	
ggg acg cca gga acg cca ggc tat act aaa gct aat tgc gtg gtc aat				739
Gly Thr Pro Gly Thr Pro Gly Tyr Thr Lys Ala Asn Cys Val Val Asn				
	60	65	70	
tgg act tct cgc acc atg ctt agc acc aat aaa aac att cct ggc cgt				787
Trp Thr Ser Arg Thr Met Leu Ser Thr Asn Lys Asn Ile Pro Gly Arg				
	75	80	85	
aac cag ccg atg tat ggg cta ggt gtg atg acg ggc tat aag cat ttt				835
Asn Gln Pro Met Tyr Gly Leu Gly Val Met Thr Gly Tyr Lys His Phe				
	90	95	100	105
atc ggt aaa aaa agg tgg ttt ggg ttg cgc tat tac ggc ttt ttt gat				883
Ile Gly Lys Lys Arg Trp Phe Gly Leu Arg Tyr Tyr Gly Phe Phe Asp				
	110	115	120	
tat ggg cat acc aat ttc tct aac tcc agg gcc gct aac gct ata tgc				931
Tyr Gly His Thr Asn Phe Ser Asn Ser Arg Ala Ala Asn Ala Ile Ser				
	125	130	135	
cct ttc tat ttg agc gat caa aaa gcg gac atg tat act tat ggt ttt				979
Pro Phe Tyr Leu Ser Asp Gln Lys Ala Asp Met Tyr Thr Tyr Gly Phe				
	140	145	150	
ggc aca gac atg ctt ttt aac att ata gat aag cct aaa gcc acg gcc				1027
Gly Thr Asp Met Leu Phe Asn Ile Ile Asp Lys Pro Lys Ala Thr Ala				
	155	160	165	
ggg ttt ttt gtg ggc gtg aat ttt gcg ggt aac act tgg acc aat aat				1075
Gly Phe Phe Val Gly Val Asn Phe Ala Gly Asn Thr Trp Thr Asn Asn				
	170	175	180	185
cgt gtg ggg tat ttt aag gac ggg tat gtt tat ggc gtc aat acg gat				1123
Arg Val Gly Tyr Phe Lys Asp Gly Tyr Val Tyr Gly Val Asn Thr Asp				
	190	195	200	
gct gac gct tac atg act aac gct gat ggc aca atc aca tgc ggg gac				1171
Ala Asp Ala Tyr Met Thr Asn Ala Asp Gly Thr Ile Thr Cys Gly Asp				
	205	210	215	
acg acg ccg gcg agt tgt gat gtg ggg att aat cct aat agc gtc tat				1219
Thr Thr Pro Ala Ser Cys Asp Val Gly Ile Asn Pro Asn Ser Val Tyr				
	220	225	230	
acc aca gga aaa ttg aac gct aaa gtg aat cac acg att ttc caa ttt				1267
Thr Thr Gly Lys Leu Asn Ala Lys Val Asn His Thr Ile Phe Gln Phe				
	235	240	245	

CHIR0340.ST25.txt

```

tta gtg aat gtg ggc att aga act aat att ttt gaa cac cat ggc att 1315
Leu Val Asn Val Gly Ile Arg Thr Asn Ile Phe Glu His His Gly Ile
250 255 260 265

gag ttt ggt atc aaa atc ccc acg ctc cct aat tac ttt ttc aaa ggc 1363
Glu Phe Gly Ile Lys Ile Pro Thr Leu Pro Asn Tyr Phe Phe Lys Gly
270 275 280

tct act acc ata aga gcg aaa aaa caa ggc ccg cta gag aat ggc caa 1411
Ser Thr Thr Ile Arg Ala Lys Lys Gln Gly Pro Leu Glu Asn Gly Gln
285 290 295

cca acc act atc acc gga gca gaa acc aat ttc agc tta acc caa acc 1459
Pro Thr Thr Ile Thr Gly Ala Glu Thr Asn Phe Ser Leu Thr Gln Thr
300 305 310

tta cgc cgt caa tat tct atg tat ttg cgc tat gtt tat act ttt tga 1507
Leu Arg Arg Gln Tyr Ser Met Tyr Leu Arg Tyr Val Tyr Thr Phe
315 320 325

atttggtagg gtttttaggc agggccttata gcttatatat ggatatatga aagcttgatt 1567

tgtcaagcct taggggtgtc attgagttgc aataactctg tgctgttttc tacttttttg 1627

ataaaatcat taatggcata acagcgtatg ttaatatgtt ctttgaaatg ggcaaattccc 1687

gcatattctt tggcgtcatc atggatatatt ggagctacaa aaacactaaa tttttctcta 1747

atatcagtgc tttttttaat caattctttt aaatgtctgg caataggtat catttccaag 1807

gtactttgac ttctatctct aatcaagctc acttctatat aactttgggc ttttgtgtcc 1867

atagctacaa tatcaggttt gttaccgctt gctgtgtata cgggcaagcc ttcattcatcg 1927

cttttataat tgggtatcac gcttaaattt tcaaaatggt gtttcaagaa aatagcgctt 1987

aaaaattcta agcgtaaagg tttatcaatg agtcttaaaa aactatcttt tgattcttgc 2047

ttgttgcaag taatgagtaa ttcttgcttg ataaaatctt tagtataagt gggtgctagt 2107

tcattcaatt tgcttgtttt aacgctctca tcagcgctga ttggagtaac gctaacaaga 2167

aagctatcca cgatc 2182

```

<210> 35

<211> 387

<212> PRT

<213> *Helicobacter pylori*

<400> 35

```

Met Leu Asn Phe Met Thr Lys Lys Lys Asn Arg Met Gln Asp Cys Lys
1 5 10 15
Met Val Gly Lys Asn Phe Asn Arg Lys Glu Ser Val Leu Ile Ala Gln
20 25 30
Ser Leu Glu Ile Ser Lys Lys Gly Ser Val Ile Leu Gly Ala Leu Leu
35 40 45
Ser Ser Leu Trp Leu Thr Asn Pro Leu Asn Ala His Glu Lys Asn Gly
50 55 60
Ala Phe Val Gly Ile Ser Leu Glu Val Gly Arg Ala Asp Gln Lys Thr
65 70 75 80
Asn Ala Tyr Arg Asn Gly Glu Leu Phe Gln Val Pro Phe Gly Asp Val
85 90 95
Ser Ala Asn Asp Asp Gly Lys Val Pro Asn Gly Gln Thr Gly Gly Cys
100 105 110
Gln Pro Ala Ser Gly Thr Pro Gly Thr Pro Gly Tyr Thr Lys Ala Asn
115 120 125
Cys Val Val Asn Trp Thr Ser Arg Thr Met Leu Ser Thr Asn Lys Asn
130 135 140
Ile Pro Gly Arg Asn Gln Pro Met Tyr Gly Leu Gly Val Met Thr Gly

```

CHIRO340.ST25.txt

```

145      150      155      160
Tyr Lys His Phe Ile Gly Lys Lys Arg Trp Phe Gly Leu Arg Tyr Tyr
      165      170      175
Gly Phe Phe Asp Tyr Gly His Thr Asn Phe Ser Asn Ser Arg Ala Ala
      180      185      190
Asn Ala Ile Ser Pro Phe Tyr Leu Ser Asp Gln Lys Ala Asp Met Tyr
      195      200      205
Thr Tyr Gly Phe Gly Thr Asp Met Leu Phe Asn Ile Ile Asp Lys Pro
      210      215      220
Lys Ala Thr Ala Gly Phe Phe Val Gly Val Asn Phe Ala Gly Asn Thr
225      230      235
Trp Thr Asn Asn Arg Val Gly Tyr Phe Lys Asp Gly Tyr Val Tyr Gly
      245      250      255
Val Asn Thr Asp Ala Asp Ala Tyr Met Thr Asn Ala Asp Gly Thr Ile
      260      265      270
Thr Cys Gly Asp Thr Thr Pro Ala Ser Cys Asp Val Gly Ile Asn Pro
      275      280      285
Asn Ser Val Tyr Thr Thr Gly Lys Leu Asn Ala Lys Val Asn His Thr
      290      295      300
Ile Phe Gln Phe Leu Val Asn Val Gly Ile Arg Thr Asn Ile Phe Glu
305      310      315
His His Gly Ile Glu Phe Gly Ile Lys Ile Pro Thr Leu Pro Asn Tyr
      325      330      335
Phe Phe Lys Gly Ser Thr Thr Ile Arg Ala Lys Lys Gln Gly Pro Leu
      340      345      350
Glu Asn Gly Gln Pro Thr Thr Ile Thr Gly Ala Glu Thr Asn Phe Ser
      355      360      365
Leu Thr Gln Thr Leu Arg Arg Gln Tyr Ser Met Tyr Leu Arg Tyr Val
      370      375      380
Tyr Thr Phe
385

```

<210> 36
 <211> 480
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (1)..(480)
 <223> bp mature protein; 17 kD protein from Helicobacter
 pylori

```

<400> 36
atg gaa caa agc cat caa aac ttg caa tct caa ttt ttt ata gag cat 48
Met Glu Gln Ser His Gln Asn Leu Gln Ser Gln Phe Phe Ile Glu His
1      5      10      15

atc tta caa att cta cct cac cgc tat ccc atg ctt tta gtg gat aga 96
Ile Leu Gln Ile Leu Pro His Arg Tyr Pro Met Leu Leu Val Asp Arg
      20      25      30

att ata gag tta caa gcc aat aaa aaa att gtc gct tat aag aat atc 144
Ile Ile Glu Leu Gln Ala Asn Lys Lys Ile Val Ala Tyr Lys Asn Ile
      35      40      45

act ttt aat gaa gac gtg ttt aac ggg cat ttc cct aat aag ccc att 192
Thr Phe Asn Glu Asp Val Phe Asn Gly His Phe Pro Asn Lys Pro Ile
      50      55      60

ttc ccg ggc gtt ttg atc gta gag ggc atg gcg caa acg gga ggg ttt 240
Phe Pro Gly Val Leu Ile Val Glu Gly Met Ala Gln Thr Gly Gly Phe
      65      70      75      80

tta gcc ttc act agc ttg tgg ggg ttt gac cct gaa atc gcc aaa aca 288
Leu Ala Phe Thr Ser Leu Trp Gly Phe Asp Pro Glu Ile Ala Lys Thr
      85      90      95

```

CHIR0340.ST25.txt

```

aaa atc gtg tat ttc atg acg att gat aag gtt aaa ttc cgc atc cct 336
Lys Ile Val Tyr Phe Met Thr Ile Asp Lys Val Lys Phe Arg Ile Pro
100 105 110

gta acc cca ggc gac aga tta gaa tac cat tta gaa gtc tta aag cat 384
Val Thr Pro Gly Asp Arg Leu Glu Tyr His Leu Glu Val Leu Lys His
115 120 125

aag ggc atg atc tgg caa gtg ggt ggc acg gct caa gtg gat ggc aaa 432
Lys Gly Met Ile Trp Gln Val Gly Gly Thr Ala Gln Val Asp Gly Lys
130 135 140

gtg gtc gct gaa gcc gaa ttg aaa gcc atg att gca gag aga gat taa 480
Val Val Ala Glu Ala Glu Leu Lys Ala Met Ile Ala Glu Arg Asp
145 150 155 160

```

```

<210> 37
<211> 159
<212> PRT
<213> Helicobacter pylori

```

```

<400> 37
Met Glu Gln Ser His Gln Asn Leu Gln Ser Gln Phe Phe Ile Glu His
1 5 10 15
Ile Leu Gln Ile Leu Pro His Arg Tyr Pro Met Leu Leu Val Asp Arg
20 25 30
Ile Ile Glu Leu Gln Ala Asn Lys Lys Ile Val Ala Tyr Lys Asn Ile
35 40 45
Thr Phe Asn Glu Asp Val Phe Asn Gly His Phe Pro Asn Lys Pro Ile
50 55 60
Phe Pro Gly Val Leu Ile Val Glu Gly Met Ala Gln Thr Gly Gly Phe
65 70 75 80
Leu Ala Phe Thr Ser Leu Trp Gly Phe Asp Pro Glu Ile Ala Lys Thr
85 90 95
Lys Ile Val Tyr Phe Met Thr Ile Asp Lys Val Lys Phe Arg Ile Pro
100 105 110
Val Thr Pro Gly Asp Arg Leu Glu Tyr His Leu Glu Val Leu Lys His
115 120 125
Lys Gly Met Ile Trp Gln Val Gly Gly Thr Ala Gln Val Asp Gly Lys
130 135 140
Val Val Ala Glu Ala Glu Leu Lys Ala Met Ile Ala Glu Arg Asp
145 150 155

```

```

<210> 38
<211> 42
<212> DNA
<213> Artificial Sequence

```

```

<220>
<221> misc_feature
<222> (3)
<223> N is inosine

```

```

<220>
<221> misc_feature
<222> (15)
<223> N is inosine

```

```

<220>
<221> misc_feature
<222> (30)
<223> N is inosine

```

```

<220>
<221> misc_feature
<222> (39)
<223> N is inosine

```

```

<220>
<223> Description of Artificial Sequence:  probes

<400> 38
gtnaayaaag atgtnaaaca aacytgtgcn ttggcgcnct ct
42

<210> 39
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  probes

<400> 39
ggcggctttt ttacygtggg ctatcaattr ggccaagtga tgcaa
45

<210> 40
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  probes

<400> 40
gtgacytatg aagtgcattg cgattttatg aaytttagca aagt
44

<210> 41
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  probes

<400> 41
aaagaaaaat ttaacagaac yaaacct
27

<210> 42
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (12)
<223> N is inosine

<220>
<221> misc_feature
<222> (15)
<223> N is inosine

<220>
<221> misc_feature
<222> (33)
<223> N is inosine

<220>
<221> misc_feature
<222> (42)
<223> N is inosine

<220>

```

<223> Description of Artificial Sequence: probes

<400> 42
gaaaaaaatg gngcntttgt gggcatyagc ttngagggtg gnagagctga tcaaaaa 57

<210> 43
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: probes

<400> 43
tggagcgctg cttttgtggg cgtgaattat caagtga gca t gatycaaaa tcaaacyaaa 60
atggtgaatg at 72

<210> 44
<211> 24
<212> PRT
<213> Helicobacter pylori

<400> 44
Glu Asp Asp Gly Gly Phe Phe Thr Val Gly Tyr Gln Leu Gly Gln Val
1 5 10 15
Met Gln Asp Val Gln Asn Pro Gly
20

<210> 45
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (9)
<223> Unknown Amino Acid

<220>
<223> Description of Artificial Sequence: probes

<400> 45
Val Asn Lys Asp Val Lys Gln Thr Xaa Ala Phe Gly Ala Pro
1 5 10

<210> 46
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: probes

<400> 46
Gly Gly Phe Phe Thr Val Gly Tyr Gln Leu Gly Gln Val Met Gln
1 5 10 15

<210> 47
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: probes

<400> 47

Val Thr Tyr Glu Val His Gly Asp Phe Ile Asn Phe Ser Lys Val
 1 5 10 15

<210> 48

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: probes

<400> 48

Lys Glu Lys Phe Asn Arg Thr Lys Pro
 1 5

<210> 49

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: probes

<400> 49

Glu Lys Asn Gly Ala Phe Val Gly Ile Ser Leu Glu Val Gly Arg Ala
 1 5 10 15

Asp Gln Lys

<210> 50

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: probes

<400> 50

Trp Ser Ala Ala Phe Val Gly Val Asn Tyr Gln Val Ser Met Ile Gln
 1 5 10 15

Asn Gln Thr Lys Met Val Asn Asp
 20

<210> 51

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: probes

<400> 51

Arg Asp Pro Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu Val
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Trp Asn Trp Asp Tyr Arg Ala
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1 5 10 15

His Thr Lys Lys Lys Lys
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